SEQUENCE LISTING

<110> Willson, Tracy
Nicola, Nicos A.
Hilton, Douglas J.
Metcalf, Donald
Zhang, Jian G.

<120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME

<130> Davies Collison Cave

<140> 09/688,286
<141> 2000-10-13

<150> 09/051,843
<151> 1998-06-29

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<170> PatentIn Ver. 2.0

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Met Ala Arg Pro Ala Leu Leu Gly Glu Leu Leu Val Leu Leu Leu Trp
  1               5                  10                  15

acc gcc acc gtg nnn ggc caa gtt gcc gcg gcc aca gaa gtt cag cca   156
Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
             20                  25                  30

cct gtg acg aat ttg agc gtc tct gtc gaa aat ctc tgc acg ata ata   204
Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile
         35                  40                  45

tgg acg tgg agt cct cct gaa gga gcc agt cca aat tgc act ctc aga   252
Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
     50                  55                  60

tat ttt agt cac ttt gat gac caa cag gat aag aaa att gct cca gaa   300
Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 65                  70                  75                  80

act cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag   348
Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
                 85                  90                  95

gtg ggc tct cag tgt agt gcc aat gaa agt gag aag cct agc cct ttg   396
Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
            100                 105                 110
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act gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc   492
Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
    130                 135                 140

tgg ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac   540
Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
145                 150                 155                 160

tat tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat   588
Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
                165                 170                 175

aga gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa   636
Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
            180                 185                 190

cct nnn agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat   684
Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
        195                 200                 205

gct ggg aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat   732
Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
    210                 215                 220

gtg aaa cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt   780
Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
225                 230                 235                 240

gcc tta tta gtg cag tgg aag aat cca caa aat ttt aga agc aga tgc   828
Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
                245                 250                 255

tta act tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat   876
Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
            260                 265                 270

att tta gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga   924
Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
        275                 280                 285

aac atg gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac   972
Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp
    290                 295                 300

gct gtc tac aca gtc aga gta aga gtc aaa aca aac aag tta tgc ttt  1020
Ala Val Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe
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aag gag caa aac tcc acc ttc tac acc acc atg tta ctc acc att cca   1116
Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
            340                 345                 350

gtc ttt gtc gca gtg gca gtc ata atc ctc ctt ttt tac ctg aaa agg   1164
Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
        355                 360                 365

ctt aag atc att ata ttt cct cca att cct gat cct ggc aag att ttt   1212
Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
    370                 375                 380

aaa gaa atg ttt gga gac cag aat gat gat acc ctg cac tgg aag aag   1260
Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
385                 390                 395                 400

tat gac atc tat gag aaa caa tcc aaa gaa gaa acg gat tct gta gtg   1308
Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
                405                 410                 415

ctg ata gaa aac ctg aag aaa gca gct cct tgatggggag aagtgatttc     1358
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     50                  55                  60

Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu
 65                  70                  75                  80

Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
                 85                  90                  95

Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu
            100                 105                 110

Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
        115                 120                 125

Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
    130                 135                 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr
145                 150                 155                 160

Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr
                165                 170                 175

Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu
            180                 185                 190

Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn
        195                 200                 205

Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr
    210                 215                 220

Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly
225                 230                 235                 240

Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys
                245                 250                 255

Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn
            260                 265                 270

Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg
        275                 280                 285
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305                 310                 315                 320

Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly
                325                 330                 335

Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro
            340                 345                 350

Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg
        355                 360                 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
    370                 375                 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
385                 390                 395                 400

Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val
                405                 410                 415

Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro
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atg gag tgg ccg gcg cgg ctc tgc ggg ctg tgg gcg ctg ctg ctc tgc   108
Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Leu Cys
  1               5                  10                  15

gcc ggc ggc ggg ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca   156
Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
            20                  25                  30

cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata   204
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     50                  55                  60

tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa   300
Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
 65                  70                  75                  80

act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa   348
Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
                 85                  90                  95

gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg   396
Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
            100                 105                 110

gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg   444
Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
        115                 120                 125

act gag ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct   492
Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
    130                 135                 140

tgg ctc cct gga agg aat acc agt ccc gac act aac tat act ctc tac   540
Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
145                 150                 155                 160

tat tgg cac aga agc ctg gaa aaa att cat caa tgt gaa aac atc ttt   588
Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
                165                 170                 175

aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag   636
Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys
            180                 185                 190

gat tcc agt ttt gaa caa cac agt gtc caa ata atg gtc aag gat aat   684
Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn
        195                 200                 205

gca gga aaa att aaa cca tcc ttc aat ata gtg cct tta act tcc cgt   732
Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg
    210                 215                 220

gtg aaa cct gat cct cca cat att aaa aac ctc tcc ttc cac aat gat   780
Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp
225                 230                 235                 240
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cta ttt tat gaa gta gaa gtc aat aac agc caa act gag aca cat aat   876
Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn
            260                 265                 270

gtt ttc tac gtc caa gag gct aaa tgt gag aat cca gaa ttt gag aga   924
Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg
        275                 280                 285

aat gtg gag aat aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat   972
Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp
    290                 295                 300

act ttg aac aca gtc aga ata aga gtc aaa aca aat aag tta tgc tat  1020
Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
305                 310                 315                 320

gag gat gac aaa ctc tgg agt aat tgg agc caa gaa atg agt ata ggt  1068
Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly
                325                 330                 335

aag aag cgc aat tcc aca ctc tac ata acc atg tta ctc att gtt cca  1116
Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
            340                 345                 350

gtc atc gtc gca ggt gca atc ata gta ctc ctg ctt tac cta aaa agg  1164
Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
        355                 360                 365

ctc aag att att ata ttc cct cca att cct gat cct ggc aag att ttt  1212
Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
    370                 375                 380

aaa gaa atg ttt gga gac cag aat gat gat act ctg cac tgg aag aag  1260
Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
385                 390                 395                 400

tac gac atc tat gag aag caa acc aag gag gaa acc gac tct gta gtg  1308
Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
                405                 410                 415

ctg ata gaa aac ctg aag aaa gcc tct cag tgatggagat aatttatttt    1358
Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
            420                 425

taccttcact gtgaccttga gaaga                                     1383
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<213> Human IL-13 receptor alpha-chain

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Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile
        35                  40                  45

Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
    50                  55                  60

Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
65                  70                  75                  80

Thr Arg Arg Ser Ile Glu Val Pro Leu Asp Glu Arg Ile Cys Leu Gln
                85                  90                  95

Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
            100                 105                 110

Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
        115                 120                 125

Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
    130                 135                 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
145                 150                 155                 160

Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
                165                 170                 175

Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys
            180                 185                 190

Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn
        195                 200                 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg
    210                 215                 220

Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp
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Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn
260 265 270

Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg
275 280 285

Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp
290 295 300

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
305 310 315 320

Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly
325 330 335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
340 345 350

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
385 390 395 400

Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
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Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
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<213> Oligo 1480 5'

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Val Gln Pro Pro Val Thr Xaa Leu Ser Val
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<210> 11
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<213> N-term amino acid sequence of mNR4 (minor)

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<222> (24)
<223> Xaa may be any amino acid

<400> 11

Ala Ser Ile Ser Ser Ser Asp Tyr Lys Asp Asp Asp Glu Ser Arg Thr Glu
1 5 10 15

Val Gln Pro Pro Val Thr Xaa Leu Ser Val
20 25